

GAP of: us-09-488-265-27 check: 2749 from: 1 to: 437

FROMIG of: /staff/overflow/sdavid-tmp/jul02/ramirez265/US09488265.pep
sequence 27, application us/09488265
general information:

applicant: leimann, martin
applicant: lassen, soeren f
title of invention: improved phylases . . .

to: us-09-684-855-160 check: 1807 from: 1 to: 440

FROMIG of: /staff/overflow/sdavid-tmp/jul02/ramirez265/fetches/US09684855.pep
sequence 160, application us/09684855
general information:

applicant: f. hofmann-la roche ag
title of invention: continuous fermentation process
file reference: c38435/111692 . . .

Symbol comparison table: /sids/appl/gcg/gcgcore/data/rundata/dlosum62.cmp
CompCheck: 1102

Gap Weight:	3	Average Match:	2.778
Length Weight:	0	Average Mismatch:	-2.248
Quality:	2318	Length:	440
Ratio:	5.304	Gaps:	1
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

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1 = IDENTITY
. = 1

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us-09-488-265-27 x us-09-684-855-160 July 2, 2002 11:26 ..

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1 NSHSCTVDGYOCPEISHLMGQYSPFSLADESAISPDPKGCRTFVQV 50
  |||||||
1 NSHSCTVDGYOCPEISHLMGQYSPFSLADESAISPDPKGCRTFVQV 50
51 LSRHGRVPTSSSKKYSALIERIOKNATPKGYAPLKTNYNTLGADLT 100
  |||||||
51 LSRHGRVPTSSSKKYSALIERIOKNATPKGYAPLKTNYNTLGADLT 100
101 PGENOMVNSGKIFRYRYKALARNIVPFVYASGSDRYIAAEKEIEGFQS 150
  |||||||
101 PGENOMVNSGKIFRYRYKALARNIVPFVYASGSDRYIAAEKEIEGFQS 150
151 AKLADPAHQASPVINVIPEGSGYNTLDHGLCTAFEDSTSEQLGDPAEA 200
  |||||||
151 AKLADPAHQASPVINVIPEGSGYNTLDHGLCTAFEDSTSEQLGDPAEA 200
198 NETAFAPIRIRARLEALPGVNLDEDEVNIMDMCPDVTARTSDATQLSP 247
  |||||||
198 NETAFAPIRIRARLEALPGVNLDEDEVNIMDMCPDVTARTSDATQLSP 247
201 NETAFAPIRIRARLEALPGVNLDEDEVNIMDMCPDVTARTSDATQLSP 250
  |||||||
201 NETAFAPIRIRARLEALPGVNLDEDEVNIMDMCPDVTARTSDATQLSP 250
248 FCDLFTADEMWDYLOSLKYYGYGAGNPLGPAQGVGFENELIARLTHSPVQ 297
  |||||||
248 FCDLFTADEMWDYLOSLKYYGYGAGNPLGPAQGVGFENELIARLTHSPVQ 297
251 FCDLFTADEMWDYLOSLKYYGYGAGNPLGPAQGVGFENELIARLTHSPVQ 300
  |||||||
251 FCDLFTADEMWDYLOSLKYYGYGAGNPLGPAQGVGFENELIARLTHSPVQ 300
298 DHTSTNHTLDSNPATPPLNATLYADFSHDNTWYSIFFALGLYNGTKPLST 347
  |||||||
298 DHTSTNHTLDSNPATPPLNATLYADFSHDNTWYSIFFALGLYNGTKPLST 347
301 DHTSTNHTLDSNPATPPLNATLYADFSHDNTWYSIFFALGLYNGTKPLST 350
  |||||||
301 DHTSTNHTLDSNPATPPLNATLYADFSHDNTWYSIFFALGLYNGTKPLST 350
348 TSVESEIETDGYAASWTVPFAARAYEMMOCEAGGGGEGEKEPLVRYLVN 397
  |||||||
348 TSVESEIETDGYAASWTVPFAARAYEMMOCEAGGGGEGEKEPLVRYLVN 397
351 TSVESEIETDGYAASWTVPFAARAYEMMOCEAGGGGEGEKEPLVRYLVN 400
  |||||||
351 TSVESEIETDGYAASWTVPFAARAYEMMOCEAGGGGEGEKEPLVRYLVN 400
398 DRVVPLHGGGVYDKLGRCKLDLDFVEGLSFARSGGNMAECFA 437
  |||||||
398 DRVVPLHGGGVYDKLGRCKLDLDFVEGLSFARSGGNMAECFA 437
401 DRVVPLHGGGVYDKLGRCKLDLDFVEGLSFARSGGNMAECFA 440
  |||||||
401 DRVVPLHGGGVYDKLGRCKLDLDFVEGLSFARSGGNMAECFA 440

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GAP of: us-09-488-265-26 check: 9654 from: 1 to: 467

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/US09488265.pep
 sequence 26, application us/09488265
 general information:

applicant: lehmann, martin
 applicant: lassen, soren f
 title of invention: improved phytases . . .

to: us-09-273-871a-9 check: 3 from: 1 to: 467

FROMIG of: /staff_overflow/sdavid-tmp/jul02/ramirez265/fetches/US09273871a.pep
 sequence 9, application us/09273871a
 general information:

applicant: svendsen, allan
 title of invention: phytase variants
 file reference: 5618.500-us . . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/blosum62.cmp
 CompCheck: 1102

Gap Weight:	3	Average Match:	2.778
Length Weight:	0	Average Mismatch:	-2.248
Quality:	2311	Length:	467
Ratio:	4.949	Gaps:	0
Percent Similarity:	94.647	Percent Identity:	93.148

Match display thresholds for the alignment(s):
 | = IDENTITY
 : =
 . = 1

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1  MGVFVLLSIATLFGSTGIALGPRGNHSCDVTGCGYQCPEISHLWQ 50
   |||||
1  MGVFVLLSIATLFGSTGIALGPRGNHSCDVTGCGYQCPEISHLWQ 50
51  YSPFSLADESAISPDVPRKGRVTFVOVLSRHGARYPTSSKSKYSALTE 100
   |||||
51  YSPFSLADESAISPDVPRKGRVTFVOVLSRHGARYPTSSKSKYSALTE 100
51  KSPFSLADESAISPDVPRKGRVTFVOVLSRHGARYPTSSKSKYSALTE 100
   |||||
101  AIOKNATAFKGKYAFLKTYNTYTLGADDLTFEGEQOMVNSGIRKRYRKAL 150
   |||||
101  AIOKNATAFKGKYAFLKTYNTYTLGADDLTFEGEQOMVNSGIRKRYRKAL 150
151  ARKIVPFRASGSDRVIASAEKFTIEGFSQAKIADPGANPHQASPYLVNTI 200
   |||||
151  ARKIVPFRASGSDRVIASAEKFTIEGFSQAKIADPGANPHQASPYLVNTI 200
201  PEGAGYNTLHGLCTAFESEELGDDVFNFTAVFAPFIRARLEAHLPGV 250
   |||||
201  PEGAGYNTLHGLCTAFESEELGDDVFNFTAVFAPFIRARLEAHLPGV 250
251  NLTDEEDVNLMDCEPDTVARTSQSLSPFCDLTFHDEMIQDYDYLQSLG 300
   |||||
251  NLTDEEDVNLMDCEPDTVARTSQSLSPFCDLTFHDEMIQDYDYLQSLG 300
301  KYGYGAGNPLGPAQGVGFVNEILARLTHSPQDHTSTNHTLDSNPATRP 350
   |||||
301  KYGYGAGNPLGPAQGVGFVNEILARLTHSPQDHTSTNHTLDSNPATRP 350
351  LNATLYADFSHDNTMVSIFEFALGLYNGTKPLSTSVESIETDGYAASWT 400
   |||||
351  LNATLYADFSHDNTMVSIFEFALGLYNGTKPLSTSVESIETDGYAASWT 400
401  VPFARAYVEMMOCBAEKELVRLVNDRVVPLHGCYVDKLGRCRKDDFV 450
   |||||
401  VPFARAYVEMMOCBAEKELVRLVNDRVVPLHGCYVDKLGRCRKDDFV 450
451  EGLSFARSGGNWMEQFA 467

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|||||
 451 EGLSFARSGGNWMEQFA 467

GAP of: us-09-488-265-26 check: 9654 from: 1 to: 467

FROMIG of: /staff/overflow/sdavid-tmp/jul02/ramirez265/US09488265.pep
sequence 26, application us/09488265

general information:
applicant: lehmann, martin
applicant: lassen, soeren f
title of invention: improved phytases . . .

to: us-09-343-126b-167 check: 7552 from: 1 to: 441

FROMIG of: /staff/overflow/sdavid-tmp/jul02/ramirez265/fetches/US09343126B.pep
sequence 167, application us/09343126b

general information:
applicant: brugger, roland
applicant: lehmann, martin
applicant: wyss, markus . . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/biosum62.cmp
Compcheck: 1102

Gap Weight:	3	Average Match:	2.778
Length Weight:	0	Average Mismatch:	-2.248
Quality:	2344	Length:	467
Ratio:	5.315	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

IDENTITY
: = 2
: = 1

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1  MGVFVVLISATLFGSTGSLGPRGNHSCDVTGQYQCEPEISHLWGQ 50
1  .....NSHSCDVTGQYQCEPEISHLWGQ 24
51  YSPFSLADSAISPDVPGKGRVTFVOVLSRHGARYPTSSSKKYSALIE 100
25  YSPFSLADSAISPDVPGKGRVTFVOVLSRHGARYPTSSSKKYSALIE 74
101  AIOKNATAFEGKAYAFELKTYNTLIGADLTPEEQOMVNSGJKEFYRRYKAL 150
75  AIOKNATAFEGKAYAFELKTYNTLIGADLTPEEQOMVNSGJKEFYRRYKAL 124
151  ARKIVPEVRASGSDRVATSAEKEFEGFQSAKLADPGANPHQASPVYINVII 200
125  ARKIVPEVRASGSDRVATSAEKEFEGFQSAKLADPGANPHQASPVYINVII 174
201  PEGAGYVNTLDHGLCTAFEESEIGDDVEANFTAVFAPIRARLEAHLPGV 250
175  PEGAGYVNTLDHGLCTAFEESEIGDDVEANFTAVFAPIRARLEAHLPGV 224
251  NLTEDEVVNLMDKCPEDTVARTSDATQLSPECDELFTHDEWIQYDYLQSLG 300
225  NLTEDEVVNLMDKCPEDTVARTSDATQLSPECDELFTHDEWIQYDYLQSLG 274
301  KYGYGAGNPLGPAQGYGFVNELIARLTHSPVODHTSTNHTLDSNPATFP 350
275  KYGYGAGNPLGPAQGYGFVNELIARLTHSPVODHTSTNHTLDSNPATFP 324
351  LNATLYADSFHDNTMWSIFFALGIYNGTKPLSTSVESIEETDGYAASWT 400
325  LNATLYADSFHDNTMWSIFFALGIYNGTKPLSTSVESIEETDGYAASWT 374
401  VPPAARAYVEMQCEAEKEPLVRLVNDRVVPLHGGVADKLGRCKRDEEV 450
375  VPPAARAYVEMQCEAEKEPLVRLVNDRVVPLHGGVADKLGRCKRDEEV 424
451  EGLSFARSGGNWECFA 467

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|||||
425 EGLSFARSGGNWECFA 441

GAP of: us-09-488-265-26 check: 9654 from: 1 to: 467

FROMIG of: /staff/overflow/sdavid-tmp/jul02/ramirez265/fetches/US09488265.pep
sequence 26, application us/09488265

general information:
applicant: Lehmann, martin
applicant: lassen, soren f
title of invention: improved phytases . . .

to: us-09-684-855-163 check: 9494 from: 1 to: 467

FROMIG of: /staff/overflow/sdavid-tmp/jul02/ramirez265/fetches/US09684855.pep
sequence 163, application us/09684855

general information:
applicant: f. hoffmann-la roche ag
title of invention: continuous fermentation process
file reference: C38435/111692 . . .

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/biosum62.cmp
Compcheck: 1102

Gap Weight:	3	Average Match:	2.778
Length Weight:	0	Average Mismatch:	-2.248

Quality:	2448	Length:	467
Ratio:	5.242	Gaps:	0
Percent Similarity:	99.143	Percent Identity:	98.929

Match display thresholds for the alignment(s):

1 - IDENTITY
2
1

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1 MGVEVVLSTATLFGSTGTLGPRGNSHSCDVTVDGTYQCFPEISHLWQ 50
1 MGVEVVLSTATLFGSTGTLGPRGNSHSCDVTVDGTYQCFPEISHLWGT 50
51 YSPFESLADSAISPDPKGRVTFVOVLSRHGARYPTSSSKKYSALIE 100
51 YSPFESLADSAISPDPKGRVTFVOVLSRHGARYPTSSSKKYSALIE 100
101 AIOKNMTAFKGKAAFLKTYNTLGGADLTPEEQOMVNSGIFKFRYKAL 150
101 AIOKNMTAFKGKAAFLKTYNTLGGADLTPEEQOMVNSGIFKFRYKAL 150
151 ARKIVPVRASGSDRYASAEKTEGFQSAKLADPGANPHQASPVINVI 200
151 ARKIVPVRASGSDRYASAEKTEGFQSAKLADPGANPHQASPVINVI 200
201 PEGAGYNNITDHLCTAFEESLGDDEANFTAVFAPPIRAREHLPGV 250
201 PEGAGYNNITDHLCTAFEESLGDDEANFTAVFAPPIRAREHLPGV 250
251 NLTDEDVNIMDMCPEDTVARTSDATQLSPCDLFTHDEWIQYDYLQSLG 300
251 NLTDEDVNIMDMCPEDTVARTSDATQLSPCDLFTHDEWIQYDYLQSLG 300
301 KYYGVGAGNPLGPAQGVFNELIARLTHSPVDHTSTNHTLDSNPATFP 350
301 KYYGVGAGNPLGPAQGVFNELIARLTHSPVDHTSTNHTLDSNPATFP 350
351 LNATLYADSFHDNTNVSIFPAGLYNGTKPLSTSVESIEETDGYAASWT 400
351 LNATLYADSFHDNTNVSIFPAGLYNGTKPLSTSVESIEETDGYAASWT 400
401 VFPAAARAYEMOCEAEKEPLVRLVNDRVVPLHGGVDKLGRCRKDDFV 450
401 VFPAAARAYEMOCEAEKEPLVRLVNDRVVPLHGGVDKLGRCRKDDFV 450
451 EGLSFARSGGNWECEFA 467
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451 EGLSFARSGGNWECEFA 467

